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RAW SEQUENCE LISTING

DATE: 12/04/2001

PATENT APPLICATION: US/09/855,564 ✓

TIME: 13:38:18

Input Set : N:\Crf3\RULE60\09855564.txt

Output Set: N:\CRF3\12042001\I855564.raw

3 <110> APPLICANT: Goodwin, Raymond G
 4 Din, Wanwan S.
 6 <120> TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
 8 <130> FILE REFERENCE: 2519
 10 <140> CURRENT APPLICATION NUMBER: 09/855,564
 11 <141> CURRENT FILING DATE: 2001-05-14
 13 <150> PRIOR APPLICATION NUMBER: 09/302,863
 14 <151> PRIOR FILING DATE: 1999-04-30
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1377
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Human
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (14)..(892)
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31					Met	Ser	Gly	Leu	Gly	Arg	Ser	Arg	Arg	Gly	Gly	Arg	
32					1				5					10			
34	agc	cgt	gtg	gac	cag	gag	gag	cgc	ttt	cca	cag	ggc	ctg	tgg	acg	ggg	97
35	Ser	Arg	Val	Asp	Gln	Glu	Glu	Arg	Phe	Pro	Gln	Gly	Leu	Trp	Thr	Gly	
36			15					20					25				
38	gtg	gct	atg	aga	tcc	tgc	ccc	gaa	gag	cag	tac	tgg	gat	cct	ctg	ctg	145
39	Val	Ala	Met	Arg	Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	
40			30					35					40				
42	ggt	acc	tgc	atg	tcc	tgc	aaa	acc	att	tgc	aac	cat	cag	agc	cag	cgc	193
43	Gly	Thr	Cys	Met	Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	
44		45				50				55			60				
46	acc	tgt	gca	gcc	ttc	tgc	agg	tca	ctc	agc	tgc	cgc	aag	gag	caa	ggc	241
47	Thr	Cys	Ala	Ala	Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	
48				65				70					75				
50	aag	ttc	tat	gac	cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	289
51	Lys	Phe	Tyr	Asp	His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	
52				80				85					90				
54	tgt	gga	cag	cac	cct	aag	caa	tgt	gca	tac	ttc	tgt	gag	aac	aag	ctc	337
55	Cys	Gly	Gln	His	Pro	Lys	Gln	Cys	Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	
56			95				100						105				
58	agg	agc	cca	gtg	aac	ctt	cca	cca	gag	ctc	agg	aga	cag	cgg	agt	gga	385
59	Arg	Ser	Pro	Val	Asn	Leu	Pro	Pro	Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	
60			110				115						120				
62	gaa	gtt	gaa	aac	aat	tca	gac	aac	tcg	gga	agg	tac	caa	gga	ttg	gag	433
63	Glu	Val	Glu	Asn	Asn	Ser	Asp	Asn	Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	
64		125				130				135			140				
66	cac	aga	ggc	tca	gaa	gca	agt	cca	gct	ctc	ccg	ggg	ctg	aag	ctg	agt	481
67	His	Arg	Gly	Ser	Glu	Ala	Ser	Pro	Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	

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68          145          150          155
70 gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529
71 Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
72          160          165          170
74 gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag 577
75 Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
76          175          180          185
78 agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625
79 Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
80          190          195          200
82 ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg 673
83 Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
84 205          210          215          220
86 agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721
87 Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
88          225          230          235
90 tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769
91 Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
92          240          245          250
94 ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg 817
95 Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
96          255          260          265
98 cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865
99 Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
100          270          275          280
102 cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg 912
103 Pro Ala Gln Glu Gly Gly Pro Gly Ala
104 285          290
106 aaaggaggag ggagagagat ggagaggagg ggagagagaa agagagggtgg ggagaggggga 972
108 gagagatatg aggagagaga gacagaggag gcagaaaagg agagaaacag aggagacaga 1032
110 gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gaggggaaaga 1092
112 ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152
114 gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggagggtc 1212
116 ggggcactct gagtcccagt tcccagtgc gctgtagggtc gtcacacact aaccacacgt 1272
118 gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctcctc ctggagaata 1332
120 aaaccttttg cagctgccct tcctcaaaaa aaaaaaaaaa aaaaa 1377
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124 <211> LENGTH: 293
125 <212> TYPE: PRT
126 <213> ORGANISM: Human
128 <400> SEQUENCE: 2
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130 1 5 10 15
132 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
133 20 25 30
135 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
136 35 40 45
138 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
139 50 55 60

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141 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
142 65 70 75 80
144 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
145 85 90 95
147 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
148 100 105 110
150 Asn Leu Pro Pro Glu Leu Arg Arg Glu Arg Ser Gly Glu Val Glu Asn
151 115 120 125
153 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
154 130 135 140
156 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
157 145 150 155 160
159 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
160 165 170 175
162 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
163 180 185 190
165 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
166 195 200 205
168 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
169 210 215 220
171 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
172 225 230 235 240
174 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
175 245 250 255
177 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
178 260 265 270
180 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
181 275 280 285
183 Gly Gly Pro Gly Ala
184 290
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 1057
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190 <213> ORGANISM: Human
192 <220> FEATURE:
193 <221> NAME/KEY: CDS
194 <222> LOCATION: (58)..(912)
196 <400> SEQUENCE: 3
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199 atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt 105
200 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
201 1 5 10 15
203 aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 153
204 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
205 20 25 30
207 cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 201
208 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
209 35 40 45
211 gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 249

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212 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
213      50      55      60
215 tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 297
216 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
217 65      70      75      80
219 gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 345
220 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
221      85      90      95
223 gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 393
224 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
225      100      105      110
227 aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 441
228 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
229      115      120      125
231 agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa 489
232 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
233      130      135      140
235 gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa 537
236 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
237 145      150      155      160
239 gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt 585
240 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
241      165      170      175
243 gcc cta gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac 633
244 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
245      180      185      190
247 ttt ttt ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg 681
248 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
249      195      200      205
251 gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg 729
252 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
253      210      215      220
255 agt ctg gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta 777
256 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
257 225      230      235      240
259 ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga 825
260 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
261      245      250      255
263 gat gaa ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg 873
264 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
265      260      265      270
267 gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt 922
268 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
269      275      280      285
271 acaccatgtc ttagctatt ttctccctt tctctgtacc tctaagaaga aagaatctaa 982
273 ctgaaaatac caaaaaaaaaa aaaaaaaaaa aaagatcttt aattaagcgg ccgcaagctt 1042
275 attcccttta gtgag 1057
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 285

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280 <212> TYPE: PRT
281 <213> ORGANISM: Human
283 <400> SEQUENCE: 4
284 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
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287 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
288           20           25           30
290 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
291           35           40           45
293 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
294           50           55           60
296 Ser Phe Tyr Gln Val Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
297   65           70           75           80
299 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
300           85           90           95
302 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
303           100          105          110
305 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
306           115          120          125
308 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
309           130          135          140
311 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
312 145           150          155          160
314 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
315           165          170          175
317 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
318           180          185          190
320 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
321           195          200          205
323 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
324           210          215          220
326 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
327 225           230          235          240
329 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
330           245          250          255
332 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
333           260          265          270
335 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
336           275          280          285
339 <210> SEQ ID NO: 5
340 <211> LENGTH: 232
341 <212> TYPE: PRT
342 <213> ORGANISM: human
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345 Met Ala Arg Arg Leu Trp Ile Leu Ser Leu Leu Ala Val Thr Leu Thr
346   1           5           10           15
348 Val Ala Leu Ala Ala Pro Ser Lys Ser Lys Arg Arg Thr Ser Ser Asp
349           20           25           30
351 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile

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VERIFICATION SUMMARY

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